REMARKS

Entry of the foregoing, reexamination and reconsideration of the above-identified application are respectfully requested.

New claims 25-42 have been added by this amendment. Claims 25-39 further define the DNA of claim 1. Claims 25-34 specify that the DNA is derived from *Anthophyta* or *Mangnoliophyta*, or *Dicotyledonopsida*, while claims 35-39 recite that the "DNA belongs to the group of anthocyanin 5-glucosyltransferse on a phyogenetic relationship of glycosyltransferases." Claims 39-41 have been added to recite nucleic acid molecules complementary to sequences encoding a 5GT. These claims have been added in view of the deletion of these embodiments from claims 20-22. No new matter is being added by these amendments.

Claims 2-5 and 22 have been amended to recite that the amino acid sequence is of SEQ ID NOs: 2, 4, 6, 8 or 12. These are the amino acid sequences set forth in the application. No new matter is added by these amendments.

Claim 2 has also been amended to recite "DNA" in the second line of the claim. This phrase is now consistent with the preamble. Claim 9 has been amended to delete the recitation of "or culturing." No new matter is added by these amendments.

Claims 2-5, 16-19 and 22 remain rejected under 35 U.S.C. §112, second paragraph, as allegedly being indefinite. This rejection is now moot in view of the instant amendment.

The claims were asserted to be indefinite by reciting "amino acid" but identifying SEQ ID NOs for nucleotide sequences. The claims have been amended to properly identify the SEQ ID NOs for the amino acid sequences rather than the nucleotide sequences. Claim 9 has been rejected for the recitation of "breeding." This term has been deleted from the claim. This rejection is now moot in view of the instant amendment.

Claims 2-7, 9-11, 16-19, 22-24 and 30 have been rejected under 35 U.S.C. §112, first paragraph, as allegedly not being enabled by the specification. This rejection is respectfully traversed.

The Official Action asserts that the specification enables an isolated DNA coding for a protein having 5GT activity having the sequences of SEQ ID NO: 2, 4, 6 or 8, and vectors, plants, progeny, tissues and processes including same. However, the Examiner asserts that the broader claims directed to modified proteins, proteins having at least 30 or 50% identity to the disclosed sequences or DNA that hybridizes to said sequences are not enabled. This assertion is believed to be in error.

As stated in applicants' prior response, based upon the high degree of homology of 5GT proteins between different species, one skilled in the art could identify and clone additional genes based upon the information, e.g., the sequences, provided in the specification.

One skilled in the art could readily use the sequences disclosed in the application as probes or primers to obtain the DNA encoding additional proteins having the ability to transfer a glycoside to the 5-position of a flavonoid. No undue experimentation would be

required for a person having ordinary skill in the art. As taught in the specification, there is a significant degree of homology between the different species in the amino acid sequence of the protein. The following table compares homology between various anthocyanin 5-glucosyltransferases (5GT), anthocyanin 3-glycosyltransferases (3GT) and anthocyanin 3-glucoside rhamnosyltransferase.

	Perilla 5GT	Verbena 5GT	Torenia 5GT	Petunia 5GT	Petunia 3GT	Petunia 3RT
Perilla 5GT		69%	63%	57%	23%	21%
Verbena 5GT			62%	55%	24%	21%
Torenia 5GT				49%	24%	20%
Petunia 5GT					26%	24%
Petunia 3GT						18%
Petunia 3RT						

The above calculations are based on Perilla 5GT, Verbena 5GT, Torenia 5GT and Petunia 5GT of the instant invention, and Petunia 3GT (Genbank accession number AB027454) and Petunia 3RT (Brugliera et al).

As can be seen from the Table, the amino acid sequence homology between the various 5GTs is at least 49%, and is clearly distinguishable from the 3GTs. Due to the high degree of homology, one skilled in the art could use the information provided in the instant application to identify additional species without undue experimentation. The sequences disclosed in the application could be used as probes or primers to obtain the

DNA encoding additional 5GT proteins. This process is described and was used by applicants in the Examples of the specification, *e.g.*, Examples 2-4. Once a homologous DNA is found, it can be expressed in yeast and the enzymatic activity determined, as described in the specification at pages 17-18 and 20-21.

Since the specification clearly teaches how to evaluate the DNA sequences, and such steps are within the skill of the art, no undue experimentation would be required to practice the invention as claimed. No undue experimentation would be required to find additional sequences having the specified modifications or degrees of identity and to evaluate their activity to determine whether they fall within the scope of the claims. While modifications of the enzymes by addition, deletion and/or replacement of amino acids may result in loss of enzyme activity, that activity can readily be measured and determined based upon the teachings of the specifications. The claims as written are thus enabled by the specification.

With respect to Bandurske et al which is said to have 30 and 35% overall and local similarity to SEQ ID NO:12, this protein would not fall within the scope of the claims. One skilled in the art could use the screening process to determine enzymatic activity and would thus find, as asserted in the Official Action, that the gene encodes a non-5GT protein. On page 5 of the Official Action, it states that no working examples show any modified DNA/protein sequence or having less than 100% sequence identity to one of the disclosed DNA/protein that retains 5GT activity. However, as shown in the above Table,

the sequences across different species have less than 100% sequence identity and have the same 5GT activity.

Withdrawal of the rejection is thus respectfully requested and believed to be in order.

Claims 1, 6, 7, 9-11, 20 and 21 also remain rejected under 35 U.S.C. §112, first paragraph, as allegedly not describing the invention as claimed. This rejection is respectfully traversed.

According to the Official Action, the sequences from four species are not a "representative number of the species of the claimed genus." As shown in the Table *supra* the different species share a high degree of homology. This is clearly taught by the specification since the data for the 4 species of 5GT in the Table is taken from the application. The specification further teaches how to obtain and screen DNA falling within the scope of the claims, as discussed *supra*. The specification thus clearly shows that applicants were in possession of the genus as claimed. Due to the teachings of homology, the four species are believed to be "representative." Moreover, based upon the four species, the teachings of homology and the teachings of screening for the claimed activity, one skilled in the art could clearly "recognize the identity of members of the genus," in accordance with *Eli Lilly*, as cited in the Official Action.

In view of the above, withdrawal of the rejection under §112(1) is respectfully requested and believed to be in order.

Claims 20-23 remain rejected under 35 U.S.C. §102(b) as allegedly being anticipated by Brugliera et al. This rejection is respectfully traversed.

Claims 20-22 have been amended to delete the recitations of "complementary." These claims should, therefore, be free of the prior art. It is asserted that "complementary" is "open to a wide variety of interpretations" and would include a 2-mer sequence. The claims have been amended to recite an isolated nucleic acid molecule which is "fully" complementary to the plant flavonoid 5GT sequence, as helpfully suggested by the Examiner.

With respect to claim 23, this claim requires under part (i) that the isolated nucleic acid molecule "encodes a 5GT of plant origin." Since Brugliera et al teaches a 3RT molecule rather than a 5GT, this rejection is believed to be in error.

In view of the above, withdrawal of the rejection of record is respectfully requested and believed to be in order.

Claims 1-7, 9-11, 16-24 remain rejected under 35 U.S.C. §103(a) as allegedly being unpatentable over Brugliera et al in view of Jonsson et al and Sambrook et al. This rejection is respectfully traversed.

The amino acid sequence homology between the 5GTs of the instant invention and 3GTs described in Brugliera et al is as low as about 20-26%. Due to the low degree of homology, it would be impossible for one skilled in the art to clone a DNA encoding 5GT as instantly claimed by hybridization with DNAs encoding 3GTs. As stated previously, the mere statement that sequences encoding 3RTs and 5GTs are included in the "invention" is

not an enabling disclosure of the instant invention. There is no teaching whatsoever of sequence information for a 5GT.

Similarly, Jonsson et al fails to teach or suggest any amino acid sequence for 5GT protein. Jonsson et al describes only a partially purified anthocyanin 5-O-glucosyltransferase. No purified enzyme or even partial amino acid sequence is provided in the reference.

Sambrook et al teaches nothing regarding a 5GT protein, or DNA encoding same.

Since none of the references disclose an isolated or purified nucleic acid or DNA as instantly claimed, the combination of references fails to teach the claimed invention. The combined teachings of the references fail to provide sufficient information to be used to obtain a DNA or nucleic acid as instantly claimed, since the only sequence disclosed, that of the 3RT of Brugliera, does not share sufficient homology to be used to clone a DNA as claimed using conventional hybridization techniques.

The position taken in this prior art rejection appears contrary to the assertions made in the enablement rejection under §112(1). Applicants traversal of these rejections, however, is consistent. What is missing in the prior art cited in the rejection is a sequence of sufficient homology to be used as a probe or primer to obtain DNA or nucleic acid sequences falling within the scope of applicants' claims. The specification provides four sequences, as shown in the Table *supra*, which are sufficiently homologous to be used to obtain additional sequences. None of the prior art, however, provides a nucleic acid, DNA or any sequence information that could be used in this regard.

It is respectfully submitted that all rejections have been overcome by the above amendments. Thus, a Notice of Allowance is respectfully requested.

In the event that there are any questions relating to this amendment or the application in general, it would be appreciated if the Examiner would contact the undersigned attorney by telephone at (508) 339-3684 so that prosecution of the application may be expedited.

Respectfully submitted,

BURNS, DOANE, SWECKER & MATHIS, L.L.P.

By: _____ #51,147
for: Donna M. Meuth
Registration No. 36,607

P.O. Box 1404
Alexandria, Virginia 22313-1404
(703) 836-6620

Date: January 3, 2002

Attachment to Reply and Amendment dated January 3, 2002

Marked-up Claims 2-5, 9, 20 and 22

2. (Thrice Amended) A DNA as set forth in claim 1 that codes for a protein having an amino acid sequence as shown in any one of SEQ ID NOs: [1, 3, 5, 7 or 11] 2, 4, 6, 8 or 12 and having activity that transfers a glycoside to the 5 position of a flavonoid, or a protein having an amino acid sequence modified by addition and/or deletion of one or more amino acids and/or substitutions by one or more other amino acids relative to said amino acids and maintains activity that transfers a glycoside to the 5 position of a flavonoid.

3. (Twice Amended) A DNA as set forth in claim 1 that codes for a protein having an amino acid sequence that has a sequence identity of 30% or more with an amino acid sequence as shown in any one of SEQ ID NOs: [1, 3, 5, 7 or 11] 2, 4, 6, 8 or 12, and has activity that transfers a glycoside to the 5 position of a flavonoid.

4. (Twice Amended) A DNA as set forth in claim 1 that codes for a protein having an amino acid sequence that has a sequence identity of 50% or more with an amino acid sequence as shown in any one of SEQ ID NOs: [1, 3, 5, 7 or 11] 2, 4, 6, 8 or 12, and has activity that transfers a glycoside to the 5 position of a flavonoid.

Attachment to Reply and Amendment dated January 3, 2002

Marked-up Claims 2-5, 9, 20 and 22

5. (Twice Amended) A DNA as set forth in claim 1 that codes for a protein, wherein said [gene] DNA hybridizes under conditions of 5 x SCC and 50°C with all or a portion of a nucleotide sequence that codes for an amino acid sequence as shown in any one of SEQ ID NOs: [1, 3, 5, 7 or 11] 2, 4, 6, 8 or 12, and has activity that transfers a glycoside to the 5 position of a flavonoid.

9. (Amended) A process for producing a protein comprising culturing [or breeding] a host as set forth in claim 7, and recovering a protein having activity that transfers a glycoside to the 5 position of a flavonoid from said host.

20. (Twice Amended) An isolated nucleic acid molecule comprising a sequence of nucleotides encoding [, or complementary to a sequence encoding,] a plant flavonoid-5-glucosyltransferase (5GT).

22. (Twice Amended) An isolated nucleic acid molecule according to claim 21, comprising a nucleotide sequence [, or nucleotide sequence complementary to a nucleotide sequence] as set forth in SEQ ID NOs: [7-10 or 12] 1, 3, 5, 7 or 11, or having at least 50% [a] sequence identity thereto.